1646

RAW SEQUENCE LISTING   DATE: 04/08/2002
PATENT APPLICATION: US/09/714,792   TIME: 09:15:57

Input Set : **N:\jumbos\09714792.raw.txt**
Output Set: **N:\CRF3\04082002\I714792.raw**

Does Not Comply
Corrected Diskette Needed

do edit

```
             SEQUENCE LISTING
  4 (1) GENERAL INFORMATION:
  6        (i) APPLICANT: Collins, Mary
  7                       Donaldson, Debra
  8                       Fitz, Lori
  9                       Neben, Tamlyn
 10                       Whitters, Matthew
 11                       Wood, Clive
 13      (ii) TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
 15     (iii) NUMBER OF SEQUENCES: 9
 17      (iv) CORRESPONDENCE ADDRESS:
 18           (A) ADDRESSEE: Genetics Institute, Inc.
 19           (B) STREET: 87 CambridgePark Drive
 20           (C) CITY: Cambridge
 21           (D) STATE: MA
 22           (E) COUNTRY: USA
 23           (F) ZIP: 02140
 25       (v) COMPUTER READABLE FORM:
 26           (A) MEDIUM TYPE: Floppy disk
 27           (B) COMPUTER: IBM PC compatible
 28           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 29           (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 31      (vi) CURRENT APPLICATION DATA:
C--> 32           (A) APPLICATION NUMBER: US/09/714,792
C--> 33           (B) FILING DATE: 16-Nov-2000
 34           (C) CLASSIFICATION:
 36    (viii) ATTORNEY/AGENT INFORMATION:
 37           (A) NAME: Brown, Scott A.
 38           (B) REGISTRATION NUMBER: 32,724
 39           (C) REFERENCE/DOCKET NUMBER: GI5268
 41      (ix) TELECOMMUNICATION INFORMATION:
 42           (A) TELEPHONE: (617) 498-8224
 43           (B) TELEFAX: (617) 876-5851


ERRORED SEQUENCES

 46 (2) INFORMATION FOR SEQ ID NO: 1:
 48        (i) SEQUENCE CHARACTERISTICS:
 49           (A) LENGTH: 1525 base pairs
 50           (B) TYPE: nucleic acid
 51           (C) STRANDEDNESS: double
 52           (D) TOPOLOGY: linear
```

```
                 RAW SEQUENCE LISTING              DATE: 04/08/2002
                 PATENT APPLICATION:  US/09/714,792   TIME: 09:15:57

                 Input Set : N:\jumbos\09714792.raw.txt
                 Output Set: N:\CRF3\04082002\I714792.raw
```

```
      54      (ii) MOLECULE TYPE: cDNA
      56     (iii) HYPOTHETICAL: NO
      59      (ix) FEATURE:
      60           (A) NAME/KEY: CDS
      61           (B) LOCATION: 256..1404
      64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
E--> 66     GAATTCGGCA CGAGGGAGAG GAGGAGGGAA AGATAGAAAG AGAGAGAGAA
     67 AGATTGCTTG      60
E--> 69     CTACCCCTGA ACAGTGACCT CTCTCAAGAC AGTGCTTTGC TCTTCACGTA
     70 TAAGGAAGGA    120
E--> 72     AAACAGTAGA GATTCAATTT AGTGTCTAAT GTGGAAAGGA GGACAAAGAG
     73 GTCTTGTGAT    180
E--> 75     AACTGCCTGT GATAATACAT TTCTTGAGAA ACCATATTAT TGAGTAGAGC
     76 TTTCAGCACA    240
E--> 78     CTAAATCCTG GAGAA ATG GCT TTT GTG CAT ATC AGA TGC TTG TGT TTC ATT
W--> 79 291
     80                  Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile
     81                   1               5                  10
E--> 83     CTT CTT TGT ACA ATA ACT GGC TAT TCT TTG GAG ATA AAA GTT AAT CCT
W--> 84 339
     85     Leu Leu Cys Thr Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro
W--> 86           15               20                  25
E--> 88     CCT CAG GAT TTT GAA ATA TTG GAT CCT GGA TTA CTT GGT TAT CTC TAT
W--> 89 387
     90     Pro Gln Asp Phe Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr
W--> 91           30               35                  40
E--> 93     TTG CAA TGG AAA CCT CCT GTG GTT ATA GAA AAA TTT AAG GGC TGT ACA
W--> 94 435
     95     Leu Gln Trp Lys Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr
W--> 96     45               50               55                  60
E--> 98     CTA GAA TAT GAG TTA AAA TAC CGA AAT GTT GAT AGC GAC AGC TGG AAG
W--> 99 483
    100     Leu Glu Tyr Glu Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys
W--> 101                 65               70                  75
E--> 103    ACT ATA ATT ACT AGG AAT CTA ATT TAC AAG GAT GGG TTT GAT CTT AAT
W--> 104 531
    105     Thr Ile Ile Thr Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn
W--> 106                 80               85                  90
E--> 108    AAA GGC ATT GAA GGA AAG ATA CGT ACG CAT TTG TCA GAG CAT TGT ACA
W--> 109 579
    110     Lys Gly Ile Glu Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr
W--> 111           95               100                 105
E--> 113    AAT GGA TCA GAA GTA CAA AGT CCA TGG ATA GAA GCT TCT TAT GGG ATA
W--> 114 627
    115     Asn Gly Ser Glu Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile
W--> 116           110              115                 120
E--> 118    TCA GAT GAA GGA AGT TTG GAA ACT AAA ATT CAG GAC ATG AAG TGT ATA
W--> 119 675
    120     Ser Asp Glu Gly Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile
```

```
W--> 121  125                    130                   135                   140
E--> 123   TAT TAT AAC TGG CAG TAT TTG GTC TGC TCT TGG AAA CCT GGC AAG ACA
W--> 124 723
     125   Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr
W--> 126                    145                   150                   155
E--> 128   GTA TAT TCT GAT ACC AAC TAT ACC ATG TTT TTC TGG TAT GAG GGC TTG
W--> 129 771
     130   Val Tyr Ser Asp Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu
W--> 131                    160                   165                   170
E--> 133   GAT CAT GCC TTA CAG TGT GCT GAT TAC CTC CAG CAT GAT GAA AAA AAT
W--> 134 819
     135   Asp His Ala Leu Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn
W--> 136                    175                   180                   185
E--> 138   GTT GGA TGC AAA CTG TCC AAC TTG GAC TCA TCA GAC TAT AAA GAT TTT
W--> 139 867
     140   Val Gly Cys Lys Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe
W--> 141         190                   195                   200
E--> 143   TTT ATC TGT GTT AAT GGA TCT TCA AAG TTG GAA CCC ATC AGA TCC AGC
W--> 144 915
     145   Phe Ile Cys Val Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser
W--> 146   205                   210                   215                   220
E--> 148   TAT ACA GTT TTT CAA CTT CAA AAT ATA GTT AAA CCA TTG CCA CCA GAA
W--> 149 963
     150   Tyr Thr Val Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu
W--> 151                    225                   230                   235
E--> 153   TTC CTT CAT ATT AGT GTG GAG AAT TCC ATT GAT ATT AGA ATG AAA TGG
W--> 154 1011
     155   Phe Leu His Ile Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp
W--> 156         240                   245                   250
E--> 158   AGC ACA CCT GGA GGA CCC ATT CCA CCA AGG TGT TAC ACT TAT GAA ATT
W--> 159 1059
     160   Ser Thr Pro Gly Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile
W--> 161         255                   260                   265
E--> 163   GTG ATC CGA GAA GAC GAT ATT TCC TGG GAG TCT GCC ACA GAC AAA AAC
W--> 164 1107
     165   Val Ile Arg Glu Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn
W--> 166         270                   275                   280
E--> 168   GAT ATG AAG TTG AAG AGG AGA GCA AAT GAA AGT GAA GAC CTA TGC TTT
W--> 169 1155
     170   Asp Met Lys Leu Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe
W--> 171   285                   290                   295                   300
E--> 173   TTT GTA AGA TGT AAG GTC AAT ATA TAT TGT GCA GAT GAT GGA ATT TGG
W--> 174 1203
     175   Phe Val Arg Cys Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp
W--> 176                    305                   310                   315
E--> 178   AGC GAA TGG AGT GAA GAG GAA TGT TGG GAA GGT TAC ACA GGG CCA GAC
W--> 179 1251
     180   Ser Glu Trp Ser Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp
W--> 181                    320                   325                   330
```

```
                RAW SEQUENCE LISTING                 DATE: 04/08/2002
                PATENT APPLICATION:  US/09/714,792   TIME: 09:15:57

                Input Set : N:\jumbos\09714792.raw.txt
                Output Set: N:\CRF3\04082002\I714792.raw


      183    TCA AAG ATT ATT TTC ATA GTA CCA GTT TGT CTT TTC TTT ATA TTC CTT      1299
      184    Ser Lys Ile Ile Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu
W--> 185            335                 340                 345
E--> 187    TTG TTA CTT CTT TGC CTT ATT GTG GAG AAG GAA GAA CCT GAA CCC ACA
W--> 188 1347
      189    Leu Leu Leu Leu Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr
W--> 190            350                 355                 360
E--> 192    TTG AGC CTC CAT GTG GAT CTG AAC AAA GAA GTG TGT GCT TAT GAA GAT
W--> 193 1395
      194    Leu Ser Leu His Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp
W--> 195            365                 370                 375                 380
E--> 197    ACC CTC TGT TAAACCACCA ATTTCTTGAC ATAGAGCCAG CCAGCAGGAG
W--> 198 1444
      199    ·Thr Leu Cys
E--> 202    TCATATTAAA CTCAATTTCT CTTAAAATTT CGAATACATC TTCTTGAAAA
      203 TCCAAAAAAA    1504
      205    AAAAAAAAAA AAAAACTCGA G                                              1525
      291 (2) INFORMATION FOR SEQ ID NO: 3:
      293        (i) SEQUENCE CHARACTERISTICS:
      294            (A) LENGTH: 1369 base pairs
      295            (B) TYPE: nucleic acid
      296            (C) STRANDEDNESS: double
      297            (D) TOPOLOGY: linear
      299      (ii) MOLECULE TYPE: cDNA
      301     (iii) HYPOTHETICAL: NO
      304      (ix) FEATURE:
      305            (A) NAME/KEY: CDS
      306            (B) LOCATION: 103..1245
      309      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
E--> 311    GGATCCGCGC GGATGAAGGC TATTTGAAGT CGCCATAACC TGGTCAGAAG
      312 TGTGCCTGTC    60
E--> 314    GGCGGGGAGA GAGGCAATAT CAAGGTTTTA AATCTCGGAG AA ATG GCT TTC
      315 GTT    114
      316                                                Met Ala Phe Val
      317                                                 1
E--> 319    TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA TTT
W--> 320 162
      321    Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr Phe
W--> 322    5                 10                  15                  20
E--> 324    GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT CAG
W--> 325 210
      326    Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro Gln
W--> 327                 25                  30                  35·
E--> 329    GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG CAA
W--> 330 258
      331    Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln
W--> 332                 40                  45                  50
E--> 334    TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG GAA
W--> 335 306
```

RAW SEQUENCE LISTING   DATE: 04/08/2002
PATENT APPLICATION: US/09/714,792   TIME: 09:15:57

Input Set : **N:\jumbos\09714792.raw.txt**
Output Set: **N:\CRF3\04082002\I714792.raw**

```
      336    Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val Glu
W--> 337         55                  60                  65
E--> 339    TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC ATC
W--> 340 354
      341    Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile
W--> 342         70                  75                  80
E--> 344    ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG GGC
W--> 345 402
      346    Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly
W--> 347         85                  90                  95                 100
E--> 349    ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT GGA
W--> 350 450
      351    Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly
W--> 352              105                 110                 115
E--> 354    TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA CCA
W--> 355 498
      356    Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro
W--> 357              120                 125                 130
E--> 359    CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT TAC
W--> 360 546
      361    Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr Tyr
W--> 362              135                 140                 145
E--> 364    AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA CTT
W--> 365 594
      366    Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val Leu
W--> 367         150                 155                 160
E--> 369    CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT CAT
W--> 370 642
      371    Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His
W--> 372    165                 170                 175                 180
E--> 374    GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA GGA
W--> 375 690
      376    Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly
W--> 377              185                 190                 195
E--> 379    TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT ATT
W--> 380 738
      381    Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile
W--> 382              200                 205                 210
E--> 384    TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT TTC
W--> 385 786
      386    Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe
W--> 387         215                 220                 225
E--> 389    ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT CTT
W--> 390 834
      391    Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Val Tyr Leu
W--> 392         230                 235                 240
E--> 394    ACT TTT ACT CGG GAG AGT TCA TGT GAA ATT AAG CTG AAA TGG AGC ATA
W--> 395 882
      396    Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile
```

```
          RAW SEQUENCE LISTING              DATE: 04/08/2002
          PATENT APPLICATION:  US/09/714,792    TIME: 09:15:57

          Input Set : N:\jumbos\09714792.raw.txt
          Output Set: N:\CRF3\04082002\I714792.raw
```

```
W--> 397   245              250              255              260
E--> 399   CCT TTG GGA CCT ATT CCA GCA AGG TGT TTT GAT TAT GAA ATT GAG ATC
W--> 400 930
     401   Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile
W--> 402                   265              270              275
E--> 404   AGA GAA GAT GAT ACT ACC TTG GTG ACT GCT ACA GTT GAA AAT GAA ACA
W--> 405 978
     406   Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val Glu Asn Glu Thr
W--> 407                   280              285              290
E--> 409   TAC ACC TTG AAA ACA ACA AAT GAA ACC CGA CAA TTA TGC TTT GTA GTA
W--> 410 1026
     411   Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu Cys Phe Val Val
W--> 412           295              300              305
E--> 414   AGA AGC AAA GTG AAT ATT TAT TGC TCA GAT GAC GGA ATT TGG AGT GAG
W--> 415 1074
     416   Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu
W--> 417       310              315              320
E--> 419   TGG AGT GAT AAA CAA TGC TGG GAA GGT GAA GAC CTA TCG AAG AAA ACT
W--> 420 1122
     421   Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr
W--> 422   325              330              335              340
E--> 424   TTG CTA CGT TTC TGG CTA CCA TTT GGT TTC ATC TTA ATA TTA GTT ATA
W--> 425 1170
     426   Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu Ile Leu Val Ile
W--> 427               345              350              355
E--> 429   TTT GTA ACC GGT CTG CTT TTG CGT AAG CCA AAC ACC TAC CCA AAA ATG
W--> 430 1218
     431   Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr Tyr Pro Lys Met
W--> 432               360              365              370
E--> 434   ATT CCA GAA TTT TTC TGT GAT ACA TGA AGACTTTCCA TATCAAGAGA
W--> 435 1265
     436   Ile Pro Glu Phe Phe Cys Asp Thr  *
W--> 437               375              380
E--> 439   CATGGTATTG ACTCAACAGT TTCCAGTCAT GGCCAAATGT TCAATATGAG
     440 TCTCAATAAA    1325
     442   CTGAATTTTT CTTGCGAAAA AAAAAAAAAA AAATCCGCGG ATCC                1369
     445 (2) INFORMATION FOR SEQ ID NO: 4:
     447      (i) SEQUENCE CHARACTERISTICS:          380
     448           (A) LENGTH: 380 amino acids      380
     449           (B) TYPE: amino acid
     450           (D) TOPOLOGY: linear
     452      (ii) MOLECULE TYPE: protein
     454      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
     456   Met Ala Phe Val Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile
     457   1               5               10              15
     459   Ser Thr Thr Phe Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val
     460           20              25              30
     462   Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
     463           35              40              45
```

RAW SEQUENCE LISTING   DATE: 04/08/2002
PATENT APPLICATION: US/09/714,792   TIME: 09:15:57

Input Set : **N:\jumbos\09714792.raw.txt**
Output Set: **N:\CRF3\04082002\I714792.raw**

```
465   Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
466       50              55              60
468   Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
469   65              70              75              80
471   Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
472           85              90              95
474   Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
475           100             105             110
477   Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
478       115             120             125
480   Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
481       130             135             140
483   Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
484   145             150             155             160
486   Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
487           165             170             175
489   Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
490       180             185             190
492   Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
493       195             200             205
495   Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
496       210             215             220
498   Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
499   225             230             235             240
501   Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
502           245             250             255
504   Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
505           260             265             270
507   Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
508       275             280             285
510   Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
511       290             295             300
513   Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
514   305             310             315             320
516   Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
517           325             330             335
519   Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
520           340             345             350
522   Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
523           355             360             365
```

E--> 525   **Tyr Pro Lys Met Ile Pro Glu Phe Phe Cys Asp Thr** (*)
E--> 526   370   375   380

VERIFICATION SUMMARY   DATE: 04/08/2002
PATENT APPLICATION: US/09/714,792   TIME: 09:15:58

Input Set : **N:\jumbos\09714792.raw.txt**
Output Set: **N:\CRF3\04082002\I714792.raw**

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:66 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:1
M:254 Repeated in SeqNo=1
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:94 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

VERIFICATION SUMMARY　　　　　　　　DATE: 04/08/2002
PATENT APPLICATION:　US/09/714,792　　TIME: 09:15:58

Input Set : **N:\jumbos\09714792.raw.txt**
Output Set: **N:\CRF3\04082002\I714792.raw**

```
L:193 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:311 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:3
M:254 Repeated in SeqNo=3
L:320 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:322 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:325 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:525 M:342 E: Invalid Stop Code On Error, STOP CODON:*
L:526 M:203 E: No. of Seq. differs, LENGTH:Input:380 Found:381 SEQ:4
L:536 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:551 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:566 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:581 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:596 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
```

STATISTICS SUMMARY   DATE: 04/08/2002
PATENT APPLICATION: **US/09/714,792**   TIME: 09:15:58

Input Set : **N:\jumbos\09714792.raw.txt**
Output Set: **N:\CRF3\04082002\I714792.raw**

Application Serial Number: US/09/714,792
Alpha or Numeric: Alpha
Application Class:
Application File Date: 11-16-2000
Art Unit: 1646
Software Application: PatentIN1.0
Total Number of Sequences: 9
Total Nucleotides: 2994
Total Amino Acids: 764
Number of Errors: 58
Number of Warnings: 100
Number of Corrections: 0

MESSAGE SUMMARY

203 **E:** 1 (No. of Seq. differs)
246 **W:** 5 (Invalid value of Alpha Sequence Header Field)
254 **E:** 56 (No. of Bases conflict)
342 **E:** 1 (Invalid Stop Code On Error)
336 **W:** 95 (Invalid Amino Acid Number in Coding Region)